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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/242,657B

DATE: 02/06/2001
TIME: 14:59:27

Input Set : A:\Sequence Listing (55411.2).txt
Output Set: N:\CRF3\02062001\I242657B.raw

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58 (vi) ORIGINAL SOURCE:
59     (A) ORGANISM: Lactococcus lactis
61 (ix) FEATURE:
62     (A) NAME/KEY: promoter
63     (B) LOCATION:26..82
64     (C) IDENTIFICATION METHOD: experimental
65     (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
66 /standard_name= "Artificial promoter library" /note= "A
67 degenerated sequence specifying a mixture of artificial
68 promoters covering a wide range of expression in small steps
69 in L. lactis"
71 (ix) FEATURE:
72     (A) NAME/KEY: misc_feature
73     (B) LOCATION:31..45
74     (D) OTHER INFORMATION:/standard_name= "Consensus
75 sequence"
77 (ix) FEATURE:
78     (A) NAME/KEY: misc_feature
79     (B) LOCATION:60..69
80     (D) OTHER INFORMATION:/standard_name= "Consensus
81 sequence"
83 (ix) FEATURE:
84     (A) NAME/KEY: misc_feature
85     (B) LOCATION:74..82
86     (D) OTHER INFORMATION:/standard_name= "Consensus
87 sequence"
89 (ix) FEATURE:
90     (A) NAME/KEY: -35_signal
91     (B) LOCATION:40..45
92     (D) OTHER INFORMATION:/standard_name= "-35 box"
94 (ix) FEATURE:
95     (A) NAME/KEY: -10_signal
96     (B) LOCATION:63..68
97     (D) OTHER INFORMATION:/standard_name= "Pribnow box"
99 (ix) FEATURE:
100    (A) NAME/KEY: misc_recomb
101    (B) LOCATION:3..25
102    (C) IDENTIFICATION METHOD: experimental
103    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
104 /standard_name= "Multiple cloning site" /label= MCS
105 /note= "A sequence specifying recognition sites
106 for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
107 MboI,
108 DpnI, AflII, MseI, SspI, NsiI."
110 (ix) FEATURE:
111     (A) NAME/KEY: misc_recomb
112     (B) LOCATION:74..98
113     (C) IDENTIFICATION METHOD: experimental
114     (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

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```

115 /standard_name= "Multiple cloning site"
116 /label= MCS
117 /note= "A sequence specifying recognition sites
118 for the restriction endonucleases: ScaI, RsaI, HpaI, HincII,
119 MseI, SfcI,
120 PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
E--> 124 CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN
125 NNNNNNNNNNT 60. → 60 format error
127 GGTATAATAN NANAGTACTG TTAAC TGCAG CTGAATT CCGG 100
129 (2) INFORMATION FOR SEQ ID NO: 2:
131     (i) SEQUENCE CHARACTERISTICS:
132         (A) LENGTH: 113 base pairs
133         (B) TYPE: nucleic acid
134         (C) STRANDEDNESS: double
135         (D) TOPOLOGY: linear
137     (ii) MOLECULE TYPE: DNA (genomic)
139     (iii) HYPOTHETICAL: YES
141     (iv) ANTI-SENSE: NO
143     (ix) FEATURE:
144         (A) NAME/KEY: promoter
145         (B) LOCATION: 23..95
146         (D) OTHER INFORMATION:/standard_name=
147 "Artificial promoter library"
148 /note= "A degenerated sequence specifying a mixture
149 of artificial temperature regulated promoters covering a wide
150 range of expression in small steps in L. lactis"
152     (ix) FEATURE:
153         (A) NAME/KEY: misc_feature
154         (B) LOCATION: 23..49
155         (D) OTHER INFORMATION:/standard_name=
156 "Sequence providing temperature regulation to promoters"
157 /note= "This sequence comprising two inverted
158 repeats separated by a short spacer provides temperature (heat
159 shock) regulation to promoters in Gram-positive bacteria"
161     (ix) FEATURE:
162         (A) NAME/KEY: misc_feature
163         (B) LOCATION: 50..60
164         (D) OTHER INFORMATION:/standard_name=
165 "Consensus sequence"
167     (ix) FEATURE:
168         (A) NAME/KEY: misc_feature
169         (B) LOCATION: 75..84
170         (D) OTHER INFORMATION:/standard_name= "Consensus
171 sequence"
173     (ix) FEATURE:
174         (A) NAME/KEY: misc_feature
175         (B) LOCATION: 89..95
176         (D) OTHER INFORMATION:/standard_name= "Consensus

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177 sequence"
179     (ix) FEATURE:
180         (A) NAME/KEY: -35_signal
181         (B) LOCATION:55..60
182         (D) OTHER INFORMATION:/standard_name= "-35 box"
184     (ix) FEATURE:
185         (A) NAME/KEY: -10_signal
186         (B) LOCATION:78..83
187         (D) OTHER INFORMATION:/standard_name= "Pribnow box"
189     (ix) FEATURE:
190         (A) NAME/KEY: misc_recomb
191         (B) LOCATION:3..22
192         (D) OTHER INFORMATION:/standard_name= "Multiple
193 cloning site"
194 /label= MCS
195 /note= "A sequence specifying recognition sites
196 for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
197 MboI, DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."
199     (ix) FEATURE:
200         (A) NAME/KEY: misc_recomb
201         (B) LOCATION:89..111
202         (D) OTHER INFORMATION:/standard_name= "Multiple
203 cloning site"
204 /label= MCS
205 /note= "A sequence specifying recognition sites
206 for the restriction endonucleases: ScaI, RsaI, SfcI, PstI,
207 Fnu4HI, BbvI,
208 PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."
210     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 212 CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNNN GAGTGCTAAT → 60
213 TTTTTGACA 60.
E--> 215 NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG → 113
W--> 216 113
218 (2) INFORMATION FOR SEQ ID NO: 3:
220     (i) SEQUENCE CHARACTERISTICS:
221         (A) LENGTH: 199 base pairs
222         (B) TYPE: nucleic acid
223         (C) STRANDEDNESS: double
224         (D) TOPOLOGY: linear
226     (ii) MOLECULE TYPE: DNA (genomic)
228     (iii) HYPOTHETICAL: YES
230     (iv) ANTI-SENSE: NO
232     (vi) ORIGINAL SOURCE:
233         (A) ORGANISM: Saccharomyces cerevisiae
235     (ix) FEATURE:
236         (A) NAME/KEY: protein_bind
237         (B) LOCATION:10..16
238         (D) OTHER INFORMATION:/function= "Activating
239 promoters in

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240 S. cerevisiae"
241 /bound_moiety= "GCN4 protein"
242 /standard_name= "Upstream activating sequence" /label=
243 UAS_GCN4p
244 /note= "A DNA sequence that specifies a binding
245 site for the GCN4 protein, which activates the transcription
246 of genes involved in amino acid synthesis in S. cerevisiae."
248 (ix) FEATURE:
249 (A) NAME/KEY: TATA_signal
250 (B) LOCATION:67..72
251 (D) OTHER INFORMATION:/standard_name= "TATA box"
253 (ix) FEATURE:
254 (A) NAME/KEY: misc_signal
255 (B) LOCATION:122..144
256 (D) OTHER INFORMATION:/function= "Transcription
257 initiation"
258 /standard_name= "T1 box"
260 (ix) FEATURE:
261 (A) NAME/KEY: protein_bind
262 (B) LOCATION:122..144
263 (D) OTHER INFORMATION:/bound_moiety= "Arginine
264 repressor"
265 /standard_name= "arginine repressor binding
266 site"
267 /label= argR
269 (ix) FEATURE:
270 (A) NAME/KEY: misc_RNA
271 (B) LOCATION:145..192
272 (D) OTHER INFORMATION:/function= "Spacer"
273 /standard_name= "Part of native sequence for
274 ARG8
275 gene incl. first codon"
277 (ix) FEATURE:
278 (A) NAME/KEY: misc_recomb
279 (B) LOCATION:3..8
280 (D) OTHER INFORMATION:/standard_name= "Recognition
281 site for restriction endonuclease EcoRI"
282 /label= EcorI_site
284 (ix) FEATURE:
285 (A) NAME/KEY: misc_recomb
286 (B) LOCATION:192..197
287 (D) OTHER INFORMATION:/standard_name= "Recognition
288 site or restriction endonuclease BamHI"
289 /label= BamHI_site
291 (ix) FEATURE:
292 (A) NAME/KEY: promoter
293 (B) LOCATION:10..192
294 (D) OTHER INFORMATION:/standard_name= "Artificial
295 promoter library"

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296 /note= "A degenerated sequence specifying a mixture
 297 of
 298 artificial promoters covering a wide range of
 299 expression in small steps in S. cerevisiae"
 301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 E--> 303 CAGAACCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 304 NNNNNNNNNN 60
same
 E--> 306 NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN NNNNNNNNNN
 307 NNNNNNNNNN 120
 E--> 309 NCTCTTAAGT GCAAGTGACT GCGAACATTT TTTTCGTTTG TTAGAATAAT
 310 TCAAGAATCG 180
 E--> 312 CTACCAATCA TGGATCCCG
 W--> 313 199
 346 (2) INFORMATION FOR SEQ ID NO: 5:
 348 (i) SEQUENCE CHARACTERISTICS:
 349 (A) LENGTH: 60 base pairs
 350 (B) TYPE: nucleic acid
 351 (C) STRANDEDNESS: double
 352 (D) TOPOLOGY: linear
 354 (ii) MOLECULE TYPE: DNA (genomic)
 356 (iii) HYPOTHETICAL: YES
 358 (iv) ANTI-SENSE: NO
 360 (vi) ORIGINAL SOURCE:
 361 (A) ORGANISM: Lactococcus lactis
 363 (ix) FEATURE:
 364 (A) NAME/KEY: promoter
 365 (B) LOCATION: 4..60
 366 (D) OTHER INFORMATION:/standard_name=
 367 "Constitutional promoter"
 368 /label= Cp1
 370 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 E--> 372 CATACCGGAG TTTATTCTTG ACAGTTCCAC CTCGGGTTGA TATAATATCT
 373 CAGTACTGTT 60
same
 375 (2) INFORMATION FOR SEQ ID NO: 6:
 377 (i) SEQUENCE CHARACTERISTICS:
 378 (A) LENGTH: 60 base pairs
 379 (B) TYPE: nucleic acid
 380 (C) STRANDEDNESS: double
 381 (D) TOPOLOGY: linear
 383 (ii) MOLECULE TYPE: DNA (genomic)
 385 (iii) HYPOTHETICAL: YES
 386 (iv) ANTI-SENSE: NO
 388 (vi) ORIGINAL SOURCE:
 389 (A) ORGANISM: Lactococcus lactis
 391 (ix) FEATURE:
 392 (A) NAME/KEY: promoter
 393 (B) LOCATION: 4..60
 394 (D) OTHER INFORMATION:/standard_name=
 395 "Constitutional promoter"

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396 /label= Cp10
398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 400 CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA
401 CAGTACTGTT 60
403 (2) INFORMATION FOR SEQ ID NO: 7:
405 (i) SEQUENCE CHARACTERISTICS:
406 (A) LENGTH: 59 base pairs
407 (B) TYPE: nucleic acid
408 (C) STRANDEDNESS: double
409 (D) TOPOLOGY: linear
411 (ii) MOLECULE TYPE: DNA (genomic)
413 (iii) HYPOTHETICAL: YES
415 (iv) ANTI-SENSE: NO
417 (vi) ORIGINAL SOURCE:
418 (A) ORGANISM: Lactococcus lactis
420 (ix) FEATURE:
421 (A) NAME/KEY: promoter
422 (B) LOCATION: 4..59
423 (D) OTHER INFORMATION:/standard_name=
424 "Constitutional promoter"
425 /label= Cp11
426 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 428 CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCCCTTGA TATAATAAGT
429 AGTACTGTT 59
431 (2) INFORMATION FOR SEQ ID NO: 8:
433 (i) SEQUENCE CHARACTERISTICS:
434 (A) LENGTH: 60 base pairs
435 (B) TYPE: nucleic acid
436 (C) STRANDEDNESS: double
437 (D) TOPOLOGY: linear
439 (ii) MOLECULE TYPE: DNA (genomic)
441 (iii) HYPOTHETICAL: YES
443 (iv) ANTI-SENSE: NO
445 (vi) ORIGINAL SOURCE:
446 (A) ORGANISM: Lactococcus lactis
447 (ix) FEATURE:
448 (A) NAME/KEY: promoter
449 (B) LOCATION: 4..60
450 (D) OTHER INFORMATION:/standard_name=
451 "Constitutional promoter"
452 /label= Cp12
454 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
E--> 456 CATATACAAG TTTATTCTTG ACACTAGTCG GCCAAAATGA TATAATACCT
457 GAGTACTGTT 60
459 (2) INFORMATION FOR SEQ ID NO: 9:
461 (i) SEQUENCE CHARACTERISTICS:
462 (A) LENGTH: 60 base pairs
463 (B) TYPE: nucleic acid
464 (C) STRANDEDNESS: double

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465 (D) TOPOLOGY: linear
 467 (ii) MOLECULE TYPE: DNA (genomic)
 469 (iii) HYPOTHETICAL: YES
 471 (iv) ANTI-SENSE: NO
 473 (vi) ORIGINAL SOURCE:
 474 (A) ORGANISM: Lactococcus lactis
 476 (ix) FEATURE:
 477 (A) NAME/KEY: promoter
 478 (B) LOCATION:4..60
 479 (D) OTHER INFORMATION:/standard_name=
 480 "Constitutional promoter"
 481 /label= Cp13
 483 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 E--> 485 CATGCTTAC TTTATTCTTG ACAAAACCAC CAGCTTTGG TATAATACGT
 486 GAGAACTGTT 60
 488 (2) INFORMATION FOR SEQ ID NO: 10:
 490 (i) SEQUENCE CHARACTERISTICS:
 491 (A) LENGTH: 60 base pairs
 492 (B) TYPE: nucleic acid
 493 (C) STRANDEDNESS: double
 494 (D) TOPOLOGY: linear
 496 (ii) MOLECULE TYPE: DNA (genomic)
 498 (iii) HYPOTHETICAL: YES
 500 (iv) ANTI-SENSE: NO
 502 (vi) ORIGINAL SOURCE:
 503 (A) ORGANISM: Lactococcus lactis
 505 (ix) FEATURE:
 506 (A) NAME/KEY: promoter
 507 (B) LOCATION:4..60
 508 (D) OTHER INFORMATION:/standard_name=
 509 "Constitutional promoter"
 510 /label= Cp14
 512 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 E--> 514 CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA
 515 CAGTACTGTT 60
 517 (2) INFORMATION FOR SEQ ID NO: 11:
 519 (i) SEQUENCE CHARACTERISTICS:
 520 (A) LENGTH: 60 base pairs
 521 (B) TYPE: nucleic acid
 522 (C) STRANDEDNESS: double
 523 (D) TOPOLOGY: linear
 525 (ii) MOLECULE TYPE: DNA (genomic)
 527 (iii) HYPOTHETICAL: YES
 529 (iv) ANTI-SENSE: NO
 531 (vi) ORIGINAL SOURCE:
 532 (A) ORGANISM: Lactococcus lactis
 534 (ix) FEATURE:
 535 (A) NAME/KEY: promoter
 536 (B) LOCATION:4..60